

Transcriptome responses of an ancient Siberian permafrost bacterium, *Psychrobacter* 273-4 to low temperature and increased osmotica

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The Siberian permafrost is an extreme, yet stable environment continually exposed to low temperature (-10°C). Ice formation increases solute concentration by decreasing the amount of free water available in the remaining water films ($a_w=0.85-0.9$).

To gain knowledge of microbial adaptation to low temperature and water activity, the genome of a Siberian permafrost isolate was sequenced. *Psychrobacter* 273-4, a gamma-*Proteobacterium* is psychroactive and displays marked physiological changes under low temperature vs. mesophilic growth and in the presence of increased osmotica.

Microarrays consisting of 70-mer oligonucleotides to the majority of predicted *Psychrobacter* genes were constructed. Differential gene expression analyses at 4°C and 22°C reveal up-regulation at 4°C for at least 10 transport genes and 9 metabolic genes including a potential amino acid metabolism operon, implicated in compatible solute production in other bacteria. The expression patterns of transport genes support physiological evidence that different carbon sources are utilized at the two temperatures. Genes involved in cation transport are down-regulated when grown in 5% NaCl,

indicating a systemic response to limit NaCl transport into the cell. Growth in salt also leads to increased glycerol-lipids and cell size due to up-regulation of these pathways. General stress response chaperones are upregulated under both increased salinity and decreased temperatures while other predicted cold responsive genes, are constitutively expressed. Several genes with unknown functions are upregulated under both stresses, indicating possible importance in stress survival. Overall, only a few members of the transcriptome changed, suggesting *Psychrobacter* 273-4 has acclimated to the low temperature, concentrated solute Siberian permafrost environment.